We Claim:

1. A composition comprising an isolated nucleic acid, wherein said nucleic acid comprises a sequence that shares at least 96% identity with SEQ ID NO:1 or the complement of SEQ ID NO:1.

2. The composition of Claim 1, wherein said sequence shares at least 97% identity with SEQ ID NO:1 or the complement of SEQ ID NO:1.

3. The composition of Claim 1, wherein said sequence shares at least 98% identity with SEQ ID NO:1 or the complement of SEQ ID NO:1.

4. The composition of Claim 1, wherein said sequence is operably linked to a heterologous promoter.

5. The composition of Claim 1, wherein said sequence is contained within a vector.

6. A composition comprising an isolated peptide encoded by the sequence of Claim 1.

7. A composition comprising an isolated nucleic acid, wherein said nucleic acid comprises a sequence encoding a peptide that shares at least 96% identity with SEQ ID NO:3.

8. The composition of Claim 7, wherein said peptide shares at least 97% identity with SEQ ID NO:3.

9. The composition of Claim 7, wherein said peptide shares at least 98% identity with SEQ ID NO:3.

10. The composition of Claim 7, wherein said sequence is operably linked to a heterologous promoter.

11. The composition of Claim 7, wherein said sequence is contained within a vector.

12. A composition comprising an isolated peptide encoded by the sequence of Claim 7.

13. A composition comprising an isolated peptide, wherein said peptide comprises an amino acid sequence that shares at least 96% identity with SEQ ID NO:3.

14. The composition of Claim 13, wherein said amino acid sequence shares at least 97% identity with SEQ ID NO:3.

15. The composition of Claim 13, wherein said amino acid sequence shares at least 98% identity with SEQ ID NO:3.

16. A composition comprising an isolated nucleic acid, wherein said nucleic acid comprises SEQ ID NO:1 or the complement of SEQ ID NO:1.

17. A composition comprising an isolated peptide, wherein said peptide comprises SEQ ID NO:3.

18. A method for determining the risk of eye disease comprising:

a) providing nucleic acid from a subject, wherein said nucleic acid comprises an LPH gene; and

b) detecting the presence or absence of at least one variation in said LPH gene.

19. The method of Claim 18, further comprising step c) providing a diagnosis to said subject based on the presence or absence of said variation.

20. The method of Claim 18, wherein said variation is a mutation.

21. The method of Claim 18, wherein said variation is a polymorphism.

22. The method of Claim 18, wherein said LPH gene is selected from human LPH1, human LPH2, and human LPH3.

23. The method of Claim 18, wherein said LPH gene is a human LPH3 sequence, and said variation prevents the peptide encoded by said human LPH3 sequence from binding the human TIGR peptide.

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